

SEQUENCE LISTING

<110> Gao, Zeren

<120> MURINE CYTOKINE RECEPTOR

<130> 00-46C1

<150> US 09/899,471

<151> 2001-07-05

<150> US 60/216,446

<151> 2000-07-06

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2256

<212> DNA

<213> Mus musculus

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<221> CDS

<222> (197)...(2218)

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caggggcgag gggctctgcc ccccttgggg gggcaggacg gggcctcagg cctgggtgct 180
gtccggcacc tggaag atg cct gtg tcc tgg ttc ctg ctg tcc ttg gca ctg 232
Met Pro Val Ser Trp Phe Leu Leu Ser Leu Ala Leu
1 5 10
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Gly Arg Asn Pro Val Val Val Ser Leu Glu Arg Leu Met Glu Pro Gln
15 20 25
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Asp Val Leu Cys Leu Pro Gly Ser Leu Gln Ser Ala Pro Gly Pro Val
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Leu Val Pro Thr Arg Leu Gln Thr Glu Leu Val Leu Arg Cys Pro Gln
65 70 75
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aag aca gat tgc gcc ctc cgt gtc cgt gtg gtg gtc cac ttg gcc gtg 472
Lys Thr Asp Cys Ala Leu Arg Val Arg Val Val Val His Leu Ala Val
80 85 90
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His Gly His Trp Ala Glu Pro Glu Glu Ala Gly Lys Ser Asp Ser Glu
95 100 105
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Leu Gln Glu Ser Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
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cac His	cag Gln	cga Arg	cgc Arg	cgt Arg	atc Ile	ctg Leu	cag Gln	gag Glu	ggt Gly	ggc Gly	gtg Val	gta Val	atc Ile	ctt Leu	ctc Leu	1816
ttc Phe	tcg Ser	ccc Pro	gcg Ala	gcc Ala	gtg Val	gcg Ala	cag Gln	tgt Cys	cag Gln	cag Gln	tgg Trp	ctg Leu	cag Gln	ctc Leu	cag Gln	1864
aca Thr	gtg Val	gag Glu	ccc Pro	ggg Gly	ccg Pro	cat His	gac Asp	gcc Ala	ctc Leu	gcc Ala	gcc Ala	tgg Trp	ctc Leu	agc Ser	tgc Cys	1912
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Arg Val Glu Arg Val Thr Gln Ala Leu Arg Ser Ala Leu Asp Ser Cys	640	645	650	
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Thr Ser Ser Ser Glu Ala Pro Gly Cys Cys Glu Glu Trp Asp Leu Gly	655	660	665	
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Cys	Ser	Leu	Gly	Leu	Ser	Cys	His	Leu	Trp	Asp	Gly	Asp	Val	Leu	Cys
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Ala	Leu	Arg	Val	Arg	Val	Val	Val	His	Leu	Ala	Val	His	Gly	His	Trp
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Tyr	Gln	Lys	Glu	Leu	Asn	Leu	Thr	Gln	Gln	Leu	Pro	Asp	Gly	Asp	Asn
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Val	Leu	Leu	Thr	Leu	Asp	Val	Ser	Glu	Glu	Gln	Asp	Phe	Ser	Phe	Leu
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Leu	Tyr	Leu	Arg	Pro	Val	Pro	Asp	Ala	Leu	Lys	Ser	Leu	Trp	Tyr	Lys
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Pro	Cys	Leu	Cys	Ile	Gln	Val	Trp	Ser	Leu	Glu	Pro	Asp	Ser	Glu	Arg
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Val	Glu	Phe	Cys	Pro	Phe	Arg	Glu	Asp	Pro	Gly	Ala	His	Arg	Asn	Leu
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325                330                335
Pro Asn Leu Cys Val Gln Val Ser Thr Trp Glu Lys Val Gln Leu Gln
340                345                350
Ala Cys Ser Trp Ala Asp Ser Leu Gly Pro Phe Lys Asp Asp Met Leu
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Glu Pro Ser Gly Cys Thr Pro Leu Pro Ser Met Ala Ser Thr Arg Ala
385                390                395                400
Ala Arg Leu Gly Glu Glu Leu Leu Gln Asp Phe Arg Ser His Gln Cys
405                410                415
Met Gln Leu Trp Asn Asp Asp Asn Met Gly Ser Leu Trp Ala Cys Pro
420                425                430
Met Asp Lys Tyr Ile His Arg Arg Trp Val Leu Val Trp Leu Ala Cys
435                440                445
Leu Leu Leu Ala Ala Ala Leu Phe Phe Phe Leu Leu Lys Lys Asp
450                455                460
Arg Arg Lys Ala Ala Arg Gly Ser Arg Thr Ala Leu Leu Leu His Ser
465                470                475                480
Ala Asp Gly Ala Gly Tyr Glu Arg Leu Val Gly Ala Leu Ala Ser Ala
485                490                495
Leu Ser Gln Met Pro Leu Arg Val Ala Val Asp Leu Trp Ser Arg Arg
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Glu Leu Ser Ala His Gly Ala Leu Ala Trp Phe His His Gln Arg Arg
515                520                525
Arg Ile Leu Gln Glu Gly Gly Val Val Ile Leu Leu Phe Ser Pro Ala
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Ala Val Ala Gln Cys Gln Gln Trp Leu Gln Leu Gln Thr Val Glu Pro
545                550                555                560
Gly Pro His Asp Ala Leu Ala Ala Trp Leu Ser Cys Val Leu Pro Asp
565                570                575
Phe Leu Gln Gly Arg Ala Thr Gly Arg Tyr Val Gly Val Tyr Phe Asp
580                585                590
Gly Leu Leu His Pro Asp Ser Val Pro Ser Pro Phe Arg Val Ala Pro
595                600                605
Leu Phe Ser Leu Pro Thr Gln Leu Pro Ala Phe Leu Asp Ala Leu Gln
610                615                620
Gly Gly Cys Ser Thr Ser Ala Gly Arg Pro Ala Asp Arg Val Glu Arg
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Leu Glu

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<210> 3

<211> 2022

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate sequence encoding the polypeptide of
SEQ ID NO:2.

<221> variation

<222> (1)...(2022)

<223> n = A, T, G or C

<400> 3

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gcnytnmgng	tnmgngtngt	ngtncaaytn	gcngtncaayg	gncaytgggc	ngarccngar	300
gargcnggna	arwsngayws	ngarytnncar	garwsnmgna	aygcwnsnyt	ncargcncar	360
ctngtnytnw	snttycargc	ntayccnath	gcnmgntgyg	cnytnytnga	rgtncargtn	420
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ccnttymgng	argayccngg	ngcncaymgn	aayytntg	ayathgcnmg	nytnmgngtn	840
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<220>

<221> CDS

<222> (197)...(2290)

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15 20 25	

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Cys	Leu	Pro	Gly	Lys	Val	Thr	Leu	Cys	Trp	Gln	Ala	Pro	Asp	Gln	Ser	
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Ala	Asp	Ser	Leu	Gly	Pro	Phe	Lys	Asp	Asp	Met	Leu	Leu	Val	Glu	Met	
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Lys	Thr	Gly	Leu	Asn	Asn	Thr	Ser	Val	Cys	Ala	Leu	Glu	Pro	Ser	Gly	
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tgt	aca	cca	ctg	ccc	agc	atg	gcc	tcc	acg	aga	gct	gct	cgc	ctg	gga	1480
Cys	Thr	Pro	Leu	Pro	Ser	Met	Ala	Ser	Thr	Arg	Ala	Ala	Arg	Leu	Gly	
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Glu	Glu	Leu	Leu	Gln	Asp	Phe	Arg	Ser	His	Gln	Cys	Met	Gln	Leu	Trp	
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Asn	Asp	Asp	Asn	Met	Gly	Ser	Leu	Trp	Ala	Cys	Pro	Met	Asp	Lys	Tyr	
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Ile	His	Arg	Arg	Trp	Val	Leu	Val	Trp	Leu	Ala	Cys	Leu	Leu	Leu	Ala	
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gcg	gcg	ctt	ttc	ttc	ttc	ctc	ctt	cta	aaa	aag	gac	cgc	agg	aaa	gcg	1672
Ala	Ala	Leu	Phe	Phe	Phe	Leu	Leu	Leu	Lys	Lys	Asp	Arg	Arg	Lys	Ala	
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Ala	Arg	Gly	Ser	Arg	Thr	Ala	Leu	Leu	Leu	His	Ser	Ala	Asp	Gly	Ala	
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Gly	Tyr	Glu	Arg	Leu	Val	Gly	Ala	Leu	Ala	Ser	Ala	Leu	Ser	Gln	Met	
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Pro	Leu	Arg	Val	Ala	Val	Asp	Leu	Trp	Ser	Arg	Arg	Glu	Leu	Ser	Ala	

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His Gly Ala Leu Ala Trp Phe His His Gln Arg Arg Arg Ile Leu Gln				
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Cys Gln Gln Trp Leu Gln Leu Gln Thr Val Glu Pro Gly Pro His Asp				
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Ala Leu Ala Ala Trp Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly				
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<212> PRT

<213> Mus musculus

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Leu Pro Gly Ser Leu Gln Ser Ala Pro Gly Pro Val Leu Val Pro Thr	
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Arg Leu Gln Thr Glu Leu Val Leu Arg Cys Pro Gln Lys Thr Asp Cys	
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Ala Leu Arg Val Arg Val Val Val His Leu Ala Val His Gly His Trp	
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Tyr	Gln	Lys	Glu	Leu	Asn	Leu	Thr	Gln	Gln	Leu	Pro	Asp	Cys	Arg	Gly
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Leu	Glu	Val	Arg	Asp	Ser	Ile	Gln	Ser	Cys	Trp	Val	Leu	Pro	Trp	Leu
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Met	Gly	Ser	Leu	Trp	Ala	Cys	Pro	Met	Asp	Lys	Tyr	Ile	His	Arg	Arg
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Trp	Val	Leu	Val	Trp	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Ala	Ala	Leu	Phe
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Phe	Phe	Leu	Leu	Leu	Lys	Lys	Asp	Arg	Arg	Lys	Ala	Ala	Arg	Gly	Ser
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Arg	Thr	Ala	Leu	Leu	His	Ser	Ala	Asp	Gly	Ala	Gly	Tyr	Glu	Arg	
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Leu	Val	Gly	Ala	Leu	Ala	Ser	Ala	Leu	Ser	Gln	Met	Pro	Leu	Arg	Val
		515					520					525			
Ala	Val	Asp	Leu	Trp	Ser	Arg	Arg	Glu	Leu	Ser	Ala	His	Gly	Ala	Leu
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Ala	Trp	Phe	His	His	Gln	Arg	Arg	Arg	Ile	Leu	Gln	Glu	Gly	Gly	Val
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Val	Ile	Leu	Leu	Phe	Ser	Pro	Ala	Ala	Val	Ala	Gln	Cys	Gln	Gln	Trp
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Leu	Gln	Leu	Gln	Thr	Val	Glu	Pro	Gly	Pro	His	Asp	Ala	Leu	Ala	Ala
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Arg Tyr Val Gly Val Tyr Phe Asp Gly Leu Leu His Pro Asp Ser Val
      610                      615          620
Pro Ser Pro Phe Arg Val Ala Pro Leu Phe Ser Leu Pro Thr Gln Leu
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Pro Ala Phe Leu Asp Ala Leu Gln Gly Gly Cys Ser Thr Ser Ala Gly
      645                      650          655
Arg Pro Ala Asp Arg Val Glu Arg Val Thr Gln Ala Leu Arg Ser Ala
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<210> 6

<211> 2094

<212> DNA

<213> Artificial Sequence

<220>

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SEQ ID NO:5.

<221> variation

<222> (1)...(2094)

<223> n = A, T, G or C

<400> 6

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 <213> Artificial Sequence

<220>
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<210> 8
 <211> 692
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr
 50 55 60
 His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys
 65 70 75 80
 Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp
 85 90 95
 Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Ser Gly
 100 105 110
 Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
 115 120 125
 Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val
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 Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr
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 Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr
 165 170 175
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 180 185 190
 Ala Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu
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 Val Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp
 210 215 220
 Asn Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr
 225 230 235 240
 Gly Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu
 245 250 255
 Cys Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile
 260 265 270
 Cys Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala
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 Ala Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro
 290 295 300
 Cys Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly

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Cys	Val	Gln	Val	Asn	Ser	Ser	Glu	Lys	Leu	Gln	Leu	Gln	Glu	Cys	Leu
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Trp	Ala	Asp	Ser	Leu	Gly	Pro	Leu	Lys	Asp	Asp	Val	Leu	Leu	Leu	Glu
						375					380				
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Ser	Arg	Ala	Leu	Gln	Pro	Ala	Leu	Asp	Ser	Tyr	Phe	His	Pro		